RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

101791,853 F

Source:

Date Processed by STIC:

ENTERED



IFWO

RAW SEQUENCE LISTING DATE: 04/21/2005 PATENT APPLICATION: US/10/791,853B TIME: 11:41:24

Input Set : E:\OP1387seqUS.txt

Output Set: N:\CRF4\04212005\J791853B.raw

3 <110> APPLICANT: TAKASHITA, Ryo YASUEDA, Hisashi GUNJI, Yoshiya 5 7 <120> TITLE OF INVENTION: METHOD FOR PRODUCING ALCOHOL BY USING MICROORGANISM W--> 9 <130> FILE REFERENCE: C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/791,853B C--> 11 <141> CURRENT FILING DATE: 2004-03-04 11 <150> PRIOR APPLICATION NUMBER: JP 2001-270903 12 <151> PRIOR FILING DATE: 2001-09-06 14 <160> NUMBER OF SEQ ID NOS: 5 16 <170> SOFTWARE: PatentIn Ver. 2.0 18 <210> SEQ ID NO: 1 19 <211> LENGTH: 38 20 <212> TYPE: DNA 21 <213> ORGANISM: Artificial Sequence 23 <220> FEATURE: 24 <223> OTHER INFORMATION: Description of Artificial Sequence:primer 26 <400> SEQUENCE: 1 27 ggtaagttta tgcagcgagt tcacactatc acggcggt 38 29 <210> SEQ ID NO: 2 30 <211> LENGTH: 30 31 <212> TYPE: DNA 32 <213> ORGANISM: Artificial Sequence 34 <220> FEATURE: 35 <223> OTHER INFORMATION: Description of Artificial Sequence:primer 37 <400> SEQUENCE: 2 38 tegaagette eeeggtteag geegeeeegg 30 40 <210> SEO ID NO: 3 41 <211> LENGTH: 39 42 <212> TYPE: DNA 43 <213> ORGANISM: Artificial Sequence 45 <220> FEATURE: 46 <223> OTHER INFORMATION: Description of Artificial Sequence:primer 48 <400> SEQUENCE: 3 39 49 cgtgaattcc cgtcggagca ttcggataac gtgctcatc 51 <210> SEQ ID NO: 4 52 <211> LENGTH: 41 53 <212> TYPE: DNA 54 <213> ORGANISM: Artificial Sequence 56 <220> FEATURE: 57 <223> OTHER INFORMATION: Description of Artificial Sequence:primer 59 <400> SEQUENCE: 4

41

60 attaagetta agegtgatag tettegaget tgeggteeag g

RAW SEQUENCE LISTING DATE: 04/21/2005 PATENT APPLICATION: US/10/791,853B TIME: 11:41:24

Input Set : E:\OP1387seqUS.txt

Output Set: N:\CRF4\04212005\J791853B.raw

```
62 <210> SEQ ID NO: 5
63 <211> LENGTH: 7188
64 <212> TYPE: DNA
65 <213> ORGANISM: Methylococcus capsulatus
67 <220> FEATURE:
68 <221> NAME/KEY: CDS
69 <222> LOCATION: (1478)..(3061)
71 <220> FEATURE:
72 <221> NAME/KEY: CDS
73 <222> LOCATION: (3142)..(4311)
75 <220> FEATURE:
76 <221> NAME/KEY: CDS
77 <222> LOCATION: (4328)..(4753)
79 <220> FEATURE:
80 <221> NAME/KEY: CDS
81 <222> LOCATION: (4764)..(5276)
83 <220> FEATURE:
84 <221> NAME/KEY: CDS
85 <222> LOCATION: (5432)..(5743)
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (5756)..(6802)
91 <400> SEQUENCE: 5
92 cggatcgttg ccggcttttc ccatcaggcc tcccgagcgg aaatggggaa gaggcggacc 60
93 teegteecca eegeetegge eagtacaegg egagagaagt getegatege ggeggtgteg 120
94 gcttcctgca ggatgtcgat cttgttcaac accaaaaaga tacggccggc gtacttccgg 180
95 accteteatg gaggaactee agtteggeet cacteaeege etggteggeg gagaggaega 240
96 acagggcggc atcgcactgc ggcacgcgcg cccaggcggt gtcggtgttg tggcggaaca 300
97 ccgagccgac gccgggtgtg tccacgatgc gcacgccatt ccccaggagc ggcgagggcg 360
98 teeggateag actteeegea egeeettege gttgeeeggg ttgeeegget eggtgatgta 420
99 atccgcgagc atatccggac ggatgtcgaa ggggctgcct tccagcggct ggacggtgat 480
100 ccggggggga tagccgtagg cgagcacggt caccaccgag gtcagcggca ccgccgcgt 540
101 gggcagcagg ttctcaccca gcagcgcgtt gatcaggctg gtcttgcccc gtttgaactg 600
102 gccgaccgtc aggacgtcga aatggccggc ctgcagcttg tcacgcaggg cgagggcggg 660
103 gcgcagagcg gcggggaggc gtccgccagc tcgtcgatca ggctcaggag ttcggttttg 720
104 agateegeat ageeggtegt tggegeetea eeggegateg geeaaegggg gategegtte 780
105 attecgcagt ggteggateg atgaeggtge ggatttegtt gategeateg gegggaaage 840
106 cgccttccag tgcgtgctgt accagcgtgg cggcgtcggg ggcaatgtag acgcagtaca 900
107 ccttgtcgtc ggtgacatag ctctcgatcc actgaacctg cggtcccatg gcgttgagga 960
108 tcgaacagga ttacgggaga tctgccgcag ttcgtcgcgc gacaggtttc cggcggccgc 1020
109 gaatcgtgcg ctctatgaca tatttgggca tggttatcag ccttacggtt ctggtaagga 1080
110 aaaaataggc ttgtattgtg cttatccgaa gataagcgct ttccgcgcag cccgattctt 1140
111 tcatggatca cgattccatt gaatgcggcg aaagtctcag ggtccggtca tgaatgaaga 1200
112 gttatggcgg cccagtacgt caccgttatg tccgatggct gtatcaaaca aagacacgtg 1260
113 tagtgatate ggacaacteg tecateceeg teggageatt eggataacgt geteategtt 1320
114 ccaaaatatt gatatacggt atacgtatcc gaagaataaa gttggcacga tccctgtaac 1380
115 taggttgtca cgacctcgtc ggaggttgta tgtccggtgt tccgtgacgt catcgggcat 1440
116 tcatcattca tagaatgtgt tacggaggaa acaagta atg gca ctt agc acc gca
117
                                             Met Ala Leu Ser Thr Ala
```

RAW SEQUENCE LISTING DATE: 04/21/2005 PATENT APPLICATION: US/10/791,853B TIME: 11:41:24

Input Set : E:\OP1387seqUS.txt

Output Set: N:\CRF4\04212005\J791853B.raw

118												1					
		_	_		_	gac Asp		-	-	-			_			-	1543
121		_		10		_			15					20			
						gtg Val											1591
123	Val	ASII	25	GIII	GIU	vai	птэ	30	пр	теп	GIII	ser	35	ASII	пр	Asp	
						acc											1639
126 127	Phe	Lys 40	Asn	Asn	Arg	Thr	Lys 45	Tyr	Ala	Thr	Lys	Tyr 50	Lys	Met	Ala	Asn	
			_	-	_	ttc	_	_		-	_	-			-	-	1687
129 130	Glu 55	Thr	Lys	Glu	Gln	Phe 60	Lys	Leu	Ile	Ala	Lys 65	Glu	Tyr	Ala	Arg	Met 70	
		gca	gtc	aag	gac	gaa	agg	cag	ttc	ggt		ctg	cag	gat	gcg		1735
						Glu											
	acc	cac	ctc	aac		ggt	att	cac	att		ccq	aaq	taa	aac		acc	1783
135						бĺу			Val								
136				90					95		~~~	~~~	+	100	~~~	-+-	1021
						aac Asn											1831
139		_	105					110			_		115				
						ctg											1879
141	ATA	120	Thr	стА	мет	Leu	125	Asp	ser	Ата	GIN	130	Ата	GIU	GIN	ьys	
143		ggc				cag	gtg					cgc					1927
		Gly	Tyr	Leu	Ala	Gln	Val	Leu	Asp	Glu		Arg	His	Thr	His		
	135 tat	acc	tac	atc	aac	140 tac	tac	ttc	aca	aaα	145 aac	aac	caq	gac	cca	150 gcc	1975
						Tyr											23.0
148					155					160					165		
						cgc Arg											2023
151	Cry	1110	71011	170	7114	71.E. G	1119	1111	175			O.L.y	110	180	110	шур	
						ttt											2071
153 154	Gly	Met	Lys 185	Arg	Val	Phe	Ser	Asp 190	Gly	Phe	Ile	Ser	Gly 195	Asp	Ala	Val	
	gaa	tgc		ctc	aac	ctg	cag		gtg	ggt	gag	gcc		ttc	acc	aat	2119
156		Cys				Leu	Gln					Ala					
157	cca	200	ato	ata	ac a	gtg	205	~ 33	+ ~~	act	000	210	220	aac	σa+	~ 22	2167
						Val											2107
160	215					220			_		225				_	230	
			-	_		ttc	_	_				-	_	_			2215
163	тте	III	PIO	1111	235	Phe	ьeu	Sel	тте	240	THE	Asp	GIU	Ten	245	nis	
164					tac	cag				tcc					ccg		2263
	Met	Ala	Asn	_	Tyr	Gln	Thr	Val		Ser	Ile	Ala	Asn		Pro	Ala	
166				250					255					260			

DATE: 04/21/2005 RAW SEQUENCE LISTING TIME: 11:41:24 PATENT APPLICATION: US/10/791,853B

Input Set : E:\OP1387seqUS.txt
Output Set: N:\CRF4\04212005\J791853B.raw

	tcc Ser							Āsp					Phe				2311
169			265					270					275				
170	cag	aag	tac	ttc	acg	ccg	gtg	ttg	ggc	atg	ctg	ttc	gag	tat	ggc	tcc	2359
	Gln																
172		280	- 1				285		4			290		-	-		
	aag		220	atc	aaa	cca		atc	220	200	taa		cac	taa	ata	tac	2407
																	2407
	Lys	Pne	гÀг	Val	GIU		пр	vai	гуз	TIIT	_	ASP	Arg	пр	var		
	295					300					305					310	
	gag	_								_	-		_			-	2455
177	Glu	Asp	Trp	Gly	Gly	Ile	Trp	Ile	Gly	Arg	Leu	Gly	Lys	Tyr	Gly	Val	
178					315					320					325		
179	gag	tcg	ccg	cgc	agc	ctc	aag	gac	gcc	aag	cag	gac	gct	tac	tgg	gct	2503
	Ğlu																
181				330			2	- 1	335	4		-		340	•		
	cac	cac	aac		tat	cta	cta	act		aca	cta	taa	cca		aac	ttc	2551
	His																2001
	nis	птз		ьeu	ıyı	ьeu	ьeu		т Ут	AIA	ьeu	пр		TIII	GIY	FIIC	
184			345					350					355				0500
	ttc																2599
186	Phe	Arg	Leu	Ala	Leu	Pro	Asp	Gln	Glu	Glu	Met		Trp	Phe	Glu	Ala	
187		360					365					370					
188	aac	tac	CCC	ggc	tgg	tac	gac	cac	tac	ggc	aag	atc	tac	gag	gaa	tgg	2647
	Asn																
	375	-		-	•	380	•		-	_	385		_			390	
	cgc	acc	cac	aat	tac		gat	cca	tcc	tca	aac	ttc	atc	cca	cta	atα	2695
	Arg																2000
	ALG	ΑΙα	Arg	Gry	395	GIU	АЗР	110	Der	400	OLY	1110	110	110	405	ricc	
193	4																2712
	tgg																2743
	Trp	Phe	TTE		Asn	Asn	His	Pro		Tyr	TTE	Asp	Arg		Ser	GIN	
196				410					415					420			
	gtg																2791
198	Val	Pro	Phe	Cys	Pro	Ser	Leu	Ala	Lys	Gly	Ala	Ser	Thr	Leu	Arg	Val	
199			425					430					435				
200	cac	qaq	tac	aac	aac	gag	atq	cac	acc	ttc	agc	gac	cag	tgg	ggc	gag	2839
	His																
202		440	- 1		2		445					450		-	-		
	cgc		taa	cta	acc	nan		gag	cac	tac	aaa		cad	aac	atc	ttc	2887
	Arg																2007
	_	Met	пр	ьeu	нта		FIO	GIU	Arg	тут		Cys	GIII	ASII	116		
	455					460					465				- 4	470	0005
	gaa																2935
	Glu	Gln	Tyr	Glu	_	Arg	Glu	Leu	Ser		Val	Ile	Ala	GLu		His	
208					475					480					485		
209	ggg	ctg	cgc	agt	gat	ggc	aag	acc	ctg	atc	gcc	cag	ccg	cat	gtc	cgt	2983
210	Gly	Leu	Arg	Ser	Asp	Gly	Lys	Thr	Leu	Ile	Ala	Gln	Pro	His	Val	Arg	
211	_		_	490	-	-	_		495					500			
	ggc	gac	aaσ		taa	acσ	tta	gac		atc	aaa	cac	cta	aac	tac	atc	3031
	Gly																
214	OTA	nsp	505	±-cu	111	1111	ыcu	510	1135	110	-y3	9	515	11011	O Y O	• • •	
	++-				~+ ~	222	~~~		~ ~ +	+~~	222	~~~+		~~~		+ a	3081
Z12	TTC	aag	aac	ccg	grg	aag	gca	rcc	aat	ıga	aacgggtgtc gggctccgtc						2001

DATE: 04/21/2005 RAW SEQUENCE LISTING PATENT APPLICATION: US/10/791,853B TIME: 11:41:24

Input Set : E:\OP1387seqUS.txt
Output Set: N:\CRF4\04212005\J791853B.raw

223 Ala Ala Val Ile Leu Lys Ala Leu Pro Glu Ala Pro Leu Asp Gly Asn 224 20 25 30 30 3285 225 aac aag atg ggt tat ttc gtc acc ccc cgc tgg aac cgc ttg acg gaa 3285 226 Asn Lys Met Gly Tyr Phe Val Thr Pro Arg Trp Lys Arg Leu Thr Glu 27 35 40 45 45 228 tat gaa gcc ctg acc gtt tat gcg cag ccc aac gcc gac tgg atc gcc 3333 229 Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala 230 50 50 55 231 ggc gcc tg gac tgg gcc gc gac tgg acc cag aaa ttc cac ggc ggc cgc 3381 232 Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg 233 65 70 80 234 cct tcc tgg ggc aac gag acc acg gag ctg cgc acc gtc gac tgg ttc 235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 85 90 95 237 aag cac cgt gac ccg ctc cgc cgt tgg cat gcc gc acc gtc aag gac 238 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp 110 240 aag gcc gac gag atc gcg cta acc gac cgc ttc ctg cag ggt tac tcc 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 242 115 120 120 125 120 243 gcc gac ggt cag atc cgg gcg atg aac ccg acc tgg cgg gac gag ttc 244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe 245 130 135 140 246 atc aac cgg tat tgg gcg ctc tc ctg ttc aac gaa tac gga ttg ttc 247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe 248 145 150 155 160 249 aac gct cat tcg cag ggc cc cgg gag gcg cc cgg ag gcg ctg cag acc cgc 250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 165 170 175 165 160 255 atc caa ctc gaa cgg ggt ttc ctc gcc aag acc cag acc acc acc ggt ttc gac acc 256 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp 257 195 200 200 215 220 220 220 225 225 225 225 225 225 22		216	Phe	Lvs	Asn	Pro	Val	Lvs	Ala	Phe	Asn								
219 atg agc atg tta gga gaa aga cgc cgc ggt ctg acc gat ccg gaa atg 220 Met Ser Met Leu Gly Glu Arg Arg Arg Gly Leu Thr Asp Pro Glu Met W> 21 1		217		520				_	525										
220 Met Ser Met Leu Gly Glu Arg Arg Arg Gly Leu Thr Asp Pro Glu Met W> 21																			
W> 221 1 5 5 Ct total and gog of the cot goal got cot got goal gog as a 223 Ala Ala Val Val Ile Leu Lys Ala Leu Pro Glu Ala Pro Leu Asp Gly Ash 224 20 20 25 30 30 3237 225 asc and at gog that the god coc coc coc coc coc total and Pro Leu Asp Gly Ash 226 Ash Lys Met Gly Tyr Phe Val Thr Pro Arg Trp Lys Arg Leu Thr Glu 227 35 40 45 228 tat goal goc cot gac got tat tegog coc coc coc coc coc got tog as coc tog god god 229 Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Ash Ala Asp Trp Ile Ala 230 50 50 50 60 231 gog coc god goc tog god coc god coc and goc god tog god god 222 Gly Gly Leu Asp Trp Gly Asp Trp Thr Glu Leu Arg Thr Val Asp Trp Phe 233 65 70 75 80 234 cot toc tog god and god coc coc god god cod god coc god 235 Pro Ser Trp Gly Ash Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 85 90 95 237 and coc cot god god cod god cod god coc god coc god god cod god and god god god god god cod god cod god god cod god god cod god god god god cod god god god god god god god god god g																			3189
222 gcg gcc gtc att ttg aag gcg ctt cct gaa gct ccg ctg gac ggc aac 223 Ala Ala Val IIe Leu Lys Ala Leu Pro Glu Ala Pro Leu Asp Gly Asn 224 20 25 30 225 aac aag atg ggt tat ttc gtc acc ccc cgc tgg aac ggt gg aac 3285 226 Asn Lys Met Gly Tyr Phe Val Thr Pro Arg Trp Lys Arg Leu Thr Glu 227 35 40 45 228 tat gaa gcc ctg acc gtt tat gcg cac cac acc gcg act gg atc gc 229 Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala 230 50 231 ggc ggc ctg gac tgg ggc gac tgg acc aag aaa ttc cac ggc ggc cgc 3381 232 Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg 233 65 70 75 80 234 cct tcc tgg ggc aac gag acc acg gag ctg gc gcc 342 235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 85 237 aag cac cgt gac cg ctc cgc cgt tgg cat ggc act gg cgc act gg gac ggc 237 238 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp 100 240 aag gcc gag gaa tgg cgc tac acc gac cgc tac gtc aag gac 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Glu Gly Tyr Ser 120 243 gcc gac ggt cag atc cgg gcg atg aac ccg acc tgg gac ag 3477 244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe 245 130 135 140 246 atc aac acc ggt ttc gac ggc gcc ttc ctg ttc acc gac gag ttc 247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Gly Tyr Gly Leu Phe 248 145 150 155 252 gtc agc ctg ctt ttg ggc gcc ttc ctg ttc aac gaa tac gac atc gcc as 250 250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 165 165 251 Road acc acc gac gg gt ttc ctg gac aac acc acc acc acc acc acc acc ac	W>			ser	мес	ьeu	G1 y	GIU	Arg	Arg	Arg		цец	1111	АЗР	110		Hec	
223 Åla Åla Val Ile Leu Lys Åla Leu Pro Glu Åla Pro Leu Asp Gly Asn 224 20 25 225 aac aag atg ggt tat ttc gtc acc ccc cgc tgg aaa cgc ttg acg gaa 226 Asn Lys Met Gly Tyr Phe Val Thr Pro Arg Trp Lys Arg Leu Thr Glu 227 35 228 tat gaa gcc ctg acc gtt tat gcg cag ccc aac gcc gac tgg atc gcc 229 Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala 230 50 55 231 ggc ggc ctg gac tgg ggc gac tgg acc ga aaa ttc cac ggc ggc cgc 232 Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg 233 65 70 75 80 234 cct tcc tgg ggc aac gag acc acg gac cg gc acc gtc gac tgg ttc 235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 85 237 aag cac cgt gac ccg ctc cgc cgt tgg cat gcc cgc tac gtc aga gac 239 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp 239 100 240 aag gcc gag gaa tgg cgt cac acc gac cgc ttc ctg cag ggt tac cc2 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 242 115 130 244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe 245 130 246 atc aac cgg tat tgg gc ccc cag gag gag gac ccc gc cg gag ga	" /		_	qcc	atc	att	ttq	aaq	qcq	ctt	cct		gct	ccg	ctg	gac		aac	3237
225 aac aag atg ggt tat tte gte acc ccc cgc tgg aaa cgc ttg acg gaa 226 Asn Lys Met Gly Tyr Phe Val Thr Pro Arg Trp Lys Arg Leu Thr Glu 45 228 tat gaa gec ctg acc ggt tat ggc cag ccc aac gcc gac tgg atc gcc 229 Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala 230 50 60 231 ggc ggc ctg gac tgg act gg acc ag acc cag aaa ttc cac ggc ggc cgc 235 Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg 233 65 70 75 80 234 cct tcc tgg ggc acc gac aga acc acg gac tg cgc acc gtc gac tgg ttc 235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 85 85 90 95 237 aag cac cgt gac ccg ctc cgc cgt tgg cat ggc cgc tgg aca gg acc gg ttc 235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 90 95 237 aag cac cgt gac ccg tcc cgc cgt tgg cat ggc cgt tat gtc aag gac 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 100 240 aag gcc gag gaa tgg cgc tac acc gac cgc ttc tg agg gg at tac tcc 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 120 243 gcc gac ggt cag atc cgg gcg ata acc ccg acc tgc gac gg ag ttc 125 244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe 130 245 130 246 atc acc cgg tat tgg ggc gcc ttc tctg ttc acc gac ggt ttc tc acc gac ggt ttc acc 247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe 150 249 acc gct cat tcg cag ggc gcc cgc gag gcg ctg tcg gac gta acc cgc 3669 250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 175 252 gtc agc ctg gct ttc tgg gac ttc gac aga atc gac acc gac aga acc acc gac aga acc acc																			
226 Asn Lys Met Gly Tyr Phe Val Thr Pro Arg Trp Lys Arg Leu Thr Glu 227 35 40 45 228 tat gaa gcc ctg acc gtt tat gcg cag ccc aac gcc gac tgg atc gcc 229 Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala 230 50 55 231 ggc ggc ctg gac tgg ggc gac tgg acc cag aaa ttc cac ggc ggc cgc 232 Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg 233 65 70 70 80 234 cct tcc tgg ggc aac gag acc acg gag ctg cgc acc gtc gac tgg ttc 235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 85 90 95 237 aag cac cgt gac ccg ccc cgt tgg cat gcc cgt acc gtc aag gac 238 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp 239 100 240 aag gcc gag gaa tgg cgc tac acc gac cgc ttc ctg cag ggt tac tcc 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 242 115 120 243 gcc gac ggt cag atc cgg gcg atg aac ccg acc tgg cgg gac gag ttc 244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe 245 130 246 atc aac cgg tat tgg ggc gcc tc tc tg ttc aac gaa tac gga ttg 247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe 248 145 150 175 252 gtc agc ctg cttc tt tgg ggc ttc gac aag atc gac atc gcc cag atg 253 Val Ser Leu Ala Phe Trp Gly Phe Asp Lys Ile Asp Ile Ala Gln Met 254 180 180 255 atc caa ctc gaa cgg gtg ttc ctc gcc aag atc gac acc ggt tc gac 256 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp 257 195 268 gag tcc aca gcg gtg ccg aag gcc cag acc gcg aac gag gtc cag acc gcg gag gtc gtc gtc gcg gag gtc gtc gtc gtc gtc gtc gtc gtc gtc gt																			
227																			3285
228 tat gaa gcc ctg acc gtt tat gcg cag ccc aac gcc gac tgg atc gcc 229 Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala 230 50 231 ggc ggc ctg gac tgg ggc gac tgg acc cag aaa ttc cac ggc ggc cgc 232 Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg 233 65 70 234 cct tcc tgg ggc aac gag acc acg gag ctg cgc acc gtc gac tgg ttc 235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 85 90 237 aag cac cgt gac ccg ctc cgc cgt tgg cat ggc cgt acg gtc aag gac 239 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp 239 100 240 aag gcc gag gaa tgg cgc tac acc gac cgc ttc ctg cag ggt tac tcc 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 242 115 120 243 gcc gac ggt cag atc cgg gg atg aac ccg acc tgg ggac gag ttc 244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe 245 130 135 246 atc aac cgg tat tgg ggc gcc ttc ctg ttc aac gaa tac gga ttg ttc 247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe 248 145 150 150 249 aac gct cat tcg cag ggc gcc cgg gag gcc cgg ag gcc cgg ag gcc cag atc cgc adc cgc 250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 251 160 252 gtc agc ctg ctg ctg ctg ggt tc ctc gca aag atc gac acc ggc atc 250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 251 165 170 252 gtc agc ctg ctg ctc tc gg acg atg acc acc aga atc gac acc ggc atg 250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 251 160 253 Val Ser Leu Ala Phe Trp Gly Phe Asp Lys Ile Asp Ile Ala Gln Met 254 180 255 atc caa ctc gaa cgg gtt tc ctc gcc aag atc gac acc ggc gat gtc cag 266 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr 260 210 270 286 aag agc cct ctt ctg gcc gtg gaa gtg ttc gac 287 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr 261 aag agc gcc ctf ctg gcc gtg gaa ggc gta tgg ag gg gtg ttc gac 288 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Pro 210 221 222 225 226			Asn	ьуs	_	GIĀ	Tyr	Pne	vaı		Pro	Arg	Trp	ьys		Leu	Thr	Glu	
229 Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala			tat	σаа		cta	acc.	att	tat		caσ	ccc	aac	acc		taa	atc	qcc	3333
231 ggc ggc ctg gac tgg ggc gac tgg acc cag aaa ttc cac ggc ggc cgc 232 GJy GJy Leu Asp Trp GJy Asp Trp Thr GJn Lys Phe His GJy GJy Arg 75 80 234 cct tcc tgg ggc aac gag acc acg gag ctg cgc acc gtc gac tgg ttc 235 Pro Ser Trp GJy Asn GJu Thr Thr GJu Leu Arg Thr Val Asp Trp Phe 95 80 236 85 90 95 237 aag cac cgt gac ccg ctc cgc cgt tgg cat ggc cgt tac gtc aag gac 234 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp 100 240 aag gcc gag gaa tgg cgc tac acc gac cgc ttc ctg cag ggt tac tcc 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln GJy Tyr Ser 115 243 gcc gac ggt cag at ccg gcg atg aac ccg acc tgc gag gac gag ttc 244 Ala Asp GJy Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe 140 245 130 135 135 140 246 atc aac cgg tat tgg ggc ctc ctc ctg ttc aac gaa tac gga ttc 247 Ile Asn Arg Tyr Trp GJy Ala Phe Leu Phe Asn GJu Tyr GJy Leu Phe 140 248 145 150 150 160 249 aac gct cat tcg cag ggc gcc cgg gag ggc ctg tcg gac gac ttc 249 aac gct cat tcg cag ggc ctg cgg gac gac gac cgc 250 Asn Ala His Ser GJn GJy Ala Arg GJu Ala Leu Ser Asp Val Thr Arg 165 252 gtc agc ctg gct ttc tgg ggc ttc gac aag atc gac acc ggt ttc gac aag atc 250 Asn Ala His Ser GJn GJy Ala Arg GJu Ala Leu Ser Asp Val Thr Arg 165 252 gtc agc ctg gct ttc tgg ggc ttc gac aag atc gac acc ggt ttc gac aag atc gac acc 250 253 Val Ser Leu Ala Phe Trp GJy Phe Asp Lys Ile Asp Ile Ala GJn Met 180 255 atc caa ctc gaa cgg gt tc ctc gcc aag atc gac acc ggt ttc gac 256 Ile GJn Leu GJu Arg GJy Phe Leu Ala Lys Ile Val Pro GJy Phe Asp 257 258 gag tca acc acc gg gt gcc gaa gcc gaa tgg acc acc gg gag gtc tac acc 250 260 210 210 215 220 261 aag agc gcc ctt ctg ctg tg gaa ggc ctg tgg cag gag gtc tcac 260 262 Lys Ser Ala Arg Leu Ala Val Glu GJy Leu Trp GJn GJu Val Phe Asp 260 262 Lys Ser Ala Arg Leu Ala Val Glu GJy Leu Trp GJn GJu Val Phe Asp 260 263 225 230																			
232 Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg 233 65 70 70 75 80 234 cct tcc tgg ggc aac gag acc acg gad ctg cgc acc gtc gac tgg ttc 235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 85 90 95 237 aag cac cgt gac ccg ctc cgc cgt tgg cat ggc ccg tac gtc aag gac 238 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp 239 100 105 240 aag gcc gag gaa tgg cgc tac acc gac cgc ttc ctg cag ggt tac tcc 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 242 115 243 gcc gac ggt cag atc cgg cga dg aac cga ccg ctc tgg cgg gac gag ttc 244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe 245 130 135 246 atc aac cgg tat tgg ggc gcc ttc ctg ttc aac gaa tac gga ttc 247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe 248 145 150 249 aac gct cat tcg cag ggc gcc ccg gag gac gcc gcc gac ga		230	-	50					55					60					
233 65																			3381
234 cct tcc tgg ggc aac gag acc acg gag ctg cgc acc gtc gac tgg ttc 235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 85 90 237 aag cac cgt gac ccg ctc cgc cgt tgg cat gcg ccg tac gtc aag gac 238 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp 239 100 240 aag gcc gag gaa tgg cgc tac acc gac cgc ttc ctg cag ggt tac tcc 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 242 115 243 gcc gac ggt cag atc cgg gcg atg aac ccg acc gac ctg ttc ctg cag ggt tac 244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Trr Trp Arg Asp Glu Phe 245 130 246 atc aac cgg tat tgg gcg cttc ctg ttc aac gaa tac gga gag ttc 247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe 248 145 249 aac gct cat tcg cag ggc gcc ctg gag gcg ctg tcg gac gac acc cgg 250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 251 252 gtc agc ctg gct ttc tgg ggc ttc gac aag atc gac acc gg ttc gac gad gac 255 Asn Caa ctc gaa cgg ggt ttc ctc gca aag acc gac acc ggt ttc gac 255 atc caa ctc gaa cgg ggt ttc ctc gca aag atc gac acc ggt ttc gac 255 Ast Caa ctc gaa cgg ggt ttc ctc gca aag atc gac acc ggt ttc gac 256 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp 257 180 258 gag tcc aca gcg gt ccg aag gcc gct ttg gac gac gag gtc tcc 250 Asn Ser Tur Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr 260 261 aag agc gcc cgt ctg ctg gaa ggc ctg ttg gaa ggg ctg ttg gac gag gtg ttc 262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp 263 225				Gly	Leu	Asp	Trp		Asp	Trp	Thr	Gln		Phe	His	Gly	GLY		
235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe 236 237 aag cac cgt gac ccg ctc cgc cgt tgg cat gcg ccg tac aga gac 3477 238 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp 100 240 aag gcc gag gaa tgg cgc tac acc gac cgc ttc ctg cag ggt tac tcc 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 120 243 gcc gac ggt cag atc cgg gg atg aac ccg acc tgg egg gac gag ttc 244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe 245 130 246 atc aac cgg tat tgg ggc gct tc ctg ttc aac gaa tac gga ttg ttc 247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe 248 145 150 249 aac gct cat tcg cag ggc gcc cgg gag ggc gct tc ctg tro gac gat acc cgc 250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 150 252 gtc agc ctg gct ttc ttg ggc ttc gac aag atc gac acc cgc 3669 255 atc cac ctc gaa cgg ggt ttc ctc gcc aag atc gac acc cgc 3717 252 gtc agc ctg gct ttc ttg ggc ttc ctg cac aag atc gac acc gg 3717 252 gtc agc ctg gct ttc ttg ggc ttc ctg cac aag atc gac acc cgc 3717 252 gtc agc ctg gct ttc ttc tgg ggc ttc gac aag atc gac acc gcc 256 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Asp Ile Ala Gln Met 180 255 atc cac ctc gac cgg ggt tc ctc gcc aag atc gac acc ggt ttc gac aag 272 acc ggt gac gat ttc 273 acc 274 acc 274 acc 275 ac				tcc	taa	aac	220	. •	200	aca	aaa	cta		acc	atc	gac	taa		3429
236																			3123
238 Lys His Arg Asp						,							5						
239		237																	3477
240 aag gcc gag gaa tgg cgc tac acc gac cgc ttc ctg cag ggt tac tcc 241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 242			Lys	His	Arg	-	Pro	Leu	Arg	Arg		His	Ala	Pro	Tyr		Lys	Asp	
241 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser 242									.			~~~	++-	a+ ~	~~~		+ > 0	+ 00	3525
242																			3323
243 gcc gac ggt cag atc cgg gcg atg aac ccg acc tgg cgg gac gag ttc 244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe 245			цуо	1114		Olu	110	**** 9			пор	9	2110	204		0-1	-1-		
245 130 135 140 246 atc aac cgg tat tgg ggc gcc ttc ctg ttc aac gaa tac gga ttg ttc 3621 247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe 248 145 150 155 160 249 aac gct cat tcg cag ggc gcc cgg gag gcg ctg ttc gac gac gta acc cgc 3669 250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 175 251 165 170 175 252 gtc agc ctg gct ttc ttgg ggc ttc gac aag atc gac atc gcc cag atg 3717 253 Val Ser Leu Ala Phe Trp Gly Phe Asp Lys Ile Asp Ile Ala Gln Met 185 190 255 atc caa ctc gaa cgg ggt ttc ctc gcc aag atc gtc ccg ggt ttc gac 3765 256 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp 200 257 195 200 258 gag tcc aca gcg gtg ccg aag gcc gaa tgg acg acg aac ggg gag gtc tac 3813 259 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr 260 210 215 261 aag agc gcc cgt ctg gcc gtg gaa ggg ctg ttg gaa ggg ctg ttc gac gag gtg ttc gac gac gag gtg ttc gac gac gac gac gac gac gac gac gac ga		243																	3573
246 atc aac cgg tat tgg ggc gcc ttc ctg ttc aac gaa tac gga ttg ttc 247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe 248 145			Ala		Gly	Gln	Ile	Arg		Met	Asn	Pro	Thr		Arg	Asp	Glu	Phe	
247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe 248 145							.			++~	~+~	++-	226		+	~~~	++~	++0	3621
248 145 150 155 160 249 aac gct cat tcg cag ggc gcc cgg gag gcg ctg tcg gac gta acc cgc 3669 250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 175 251 165 170 175 175 252 gtc agc ctg gct ttc tgg ggc ttc gac aag atc gac atc gcc cag atg 3717 253 Val Ser Leu Ala Phe Trp Gly Phe Asp Lys Ile Asp Ile Ala Gln Met 180 185 190 255 atc caa ctc gaa cgg ggt ttc ctc gcc aag atc gta ccc ggt ttc gac 3765 256 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp 205 258 gag tcc aca gcg gtg ccg aag gcc gaa tgg acg acg gag gtc tac 3813 259 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr 200 261 aag agc gcc cgt ctg gcc gtg gaa ggc gtg gaa ggg ctg ttc gac 3861 262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp 3861 263 225 230																			3021
250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg 251				11011	9	- 1 -	119					20			- 1 -	 1			
251																			3669
252 gtc agc ctg gct ttc tgg ggc ttc gac aag atc gac atc gcc cag atg 3717 253 Val Ser Leu Ala Phe Trp Gly Phe Asp Lys Ile Asp Ile Ala Gln Met 254 180 185 190 255 atc caa ctc gaa cgg ggt ttc ctc gcc aag atc gta ccc ggt ttc gac 3765 256 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp 257 195 200 205 258 gag tcc aca gcg gtg ccg aag gcc gaa tgg acg aac ggg gag gtc tac 3813 259 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr 260 210 215 220 261 aag agc gcc cgt ctg gcc gtg gaa ggg ctg tgg cag gag gtc tc gac 3861 262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp 263 225 230 235 240			Asn	Ala	His	Ser		Gly	Ala	Arg	Glu		Leu	Ser	Asp	Val		Arg	
253 Val Ser Leu Ala Phe Trp Gly Phe Asp Lys Ile Asp Ile Ala Gln Met 254								.		++-	~~~		a t a	~~~	2+2	~~~		2+4	3717
254																			3111
255 atc caa ctc gaa cgg ggt ttc ctc gcc aag atc gta ccc ggt ttc gac 3765 256 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp 257 195 200 205 258 gag tcc aca gcg gtg ccg aag gcc gaa tgg acg aac ggg gag gtc tac 3813 259 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr 260 210 215 220 261 aag agc gcc cgt ctg gcc gtg gaa ggg ctg tgg cag gag gtg ttc gac 3861 262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp 263 225 230 235 240			Vai	DCI	пса		1110	115	O±1	1110		11,0		пор					
257 195 200 205 258 gag tcc aca gcg gtg ccg aag gcc gaa tgg acg aac ggg gag gtc tac 3813 259 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr 260 210 215 220 261 aag agc gcc cgt ctg gcc gtg gaa ggg ctg tgg cag gag gtg ttc gac 3861 262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp 263 225 230 235 240		255																	3765
258 gag tcc aca gcg gtg ccg aag gcc gaa tgg acg aac ggg gag gtc tac 259 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr 260 210 215 220 261 aag agc gcc cgt ctg gcc gtg gaa ggg ctg tgg cag gag gtg ttc gac 262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp 263 225 230 235 240			Ile	Gln		Glu	Arg	Gly	Phe		Ala	Lys	Ile	Val		Gly	Phe	Asp	
259 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr 260 210 215 220 261 aag agc gcc cgt ctg gcc gtg gaa ggg ctg tgg cag gag gtg ttc gac 3861 262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp 263 225 230 235 240												.				~~~	~+~	+	2012
260 210 215 220 261 aag agc gcc cgt ctg gcc gtg gaa ggg ctg tgg cag gag gtg ttc gac 3861 262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp 263 225 230 235 240																			3013
261 aag agc gcc cgt ctg gcc gtg gaa ggg ctg tgg cag gag gtg ttc gac 3861 262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp 263 225 230 235 240			GIU		1111	нта	vaı	110		AΙα	Olu	115	1111		OL y	OLU	V 4 1	- 1 -	
262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp 263 225 230 235 240			aag		gcc	cgt	ctg	gcc		gaa	ggg	ctg	tgg		gag	gtg	ttc	gac	3861
		262	Lys	Ser	Āla	Ārg	Leu	Āla	Val	Glu	Gly	Leu	Trp	Gln	Glu	Val	Phe	Asp	
264 tag aac gag age get tte teg gtg cae gee gte tat gae geg etg tte 3909																	,		2000
		264	tgg	aac	gag	agc	gct	ttc	tcg	gtg	cac	gcc	gtc	tat	gac	gcg	ctg	ttc	3909

VERIFICATION SUMMARY

DATE: 04/21/2005 PATENT APPLICATION: US/10/791,853B TIME: 11:41:25

Input Set : E:\OP1387seqUS.txt

Output Set: N:\CRF4\04212005\J791853B.raw

```
L:9 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
 L:11 M:270 C: Current Application Number differs, Replaced Current Application No
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:293 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:320 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:326 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:329 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:332 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:341 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:344 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:347 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:350 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:353 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:361 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:373 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:376 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:388 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:391 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:394 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:397 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:400 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:406 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:409 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:412 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:418 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:421 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:424 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 L:430 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:433 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:436 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:442 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
```